

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/945,254

DATE: 09/21/2001  
TIME: 20:48:55

Input Set : A:\Seqlist.txt  
Output Set: N:\CRF3\09212001\I945254.raw

4 <110> APPLICANT: Meyers, Rachel  
5 MacBeth, Kyle  
6 Tsai, Fong-Ying  
8 <120> TITLE OF INVENTION: 8797, A NOVEL HUMAN  
9 GALACTOSYLTRANSFERASE AND USES THEREOF  
11 <130> FILE REFERENCE: MNI-188  
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/945,254  
C--> 13 <141> CURRENT FILING DATE: 2001-08-31  
13 <150> PRIOR APPLICATION NUMBER: 60/229,829  
14 <151> PRIOR FILING DATE: 2000-08-31  
16 <160> NUMBER OF SEQ ID NOS: 3  
18 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
20 <210> SEQ ID NO: 1  
21 <211> LENGTH: 4052  
22 <212> TYPE: DNA  
23 <213> ORGANISM: Homo sapiens  
25 <220> FEATURE:  
26 <221> NAME/KEY: CDS  
27 <222> LOCATION: (459)...(1592)  
29 <400> SEQUENCE: 1  
30 ccaagattta aagccgc当地 tgtagaccgc gacttagct ccgatgc当地 60  
31 aaggaaagcc gaccccgat ttggacattt aaagagctgg gcttgaactt cgttagttc 120  
32 gctctaaact gccc当地 gtaagctgg cttggagggtg gcatggaata ttcacatggg 180  
33 agagccgc当地 accacgcttc ctgaaggatg cccgtgtggg agaattttga 240  
34 cgtgccagtg tcctcgatcc acagggtgtt ccattttcc gcaatctca gaaaatggg 300  
35 ctaaaagaaa ctatttgtt aaataagaag acttc当地 ttaatgacca acatgtatta 360  
36 agatggacac ctactctacg aaacacgaaat ttctatggtc tc当地 gaaagc ccgtgc当地 420  
37 ttaaaactga tccttaactaa aaacagactt gagtgatg atg aga atg tt当地 gtt agt 476  
38 Met Arg Met Leu Val Ser  
39 1 5  
41 ggc aga aga gtc aaa aaa tgg cag tta att att cag tta ttt gct act 524  
42 Gly Arg Arg Val Lys Lys Trp Gln Leu Ile Ile Gln Leu Phe Ala Thr  
43 10 15 20  
45 tgt ttt tta gcg agc ctc atg ttt ttt tgg gaa cca atc gat aat cac 572  
46 Cys Phe Leu Ala Ser Leu Met Phe Phe Trp Glu Pro Ile Asp Asn His  
47 25 30 35  
49 att gtg agc cat atg aag tca tat tct tac aga tac ctc ata aat agc 620  
50 Ile Val Ser His Met Lys Ser Tyr Ser Tyr Arg Tyr Leu Ile Asn Ser  
51 40 45 50  
53 tat gac ttt gtg aat gat acc ctg tct ctt aag cac acc tca gcg ggg 668  
54 Tyr Asp Phe Val Asn Asp Thr Leu Ser Leu Lys His Thr Ser Ala Gly  
55 55 60 65 70  
57 cct cgc tac caa tac ttg att aac cac aag gaa aag tgt caa gct caa 716  
58 Pro Arg Tyr Gln Tyr Leu Ile Asn His Lys Glu Lys Cys Gln Ala Gln  
59 75 80 85  
61 gac gtc ctc ctt tta ctg ttt gta aaa act gct cct gaa aac tat gat 764  
62 Asp Val Leu Leu Leu Phe Val Lys Thr Ala Pro Glu Asn Tyr Asp

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63	90	95	100	
65	cga cgt tcc gga att aga agg acg tgg ggc aat gaa aat tat gtt cg	812		
66	Arg Arg Ser Gly Ile Arg Arg Thr Trp Gly Asn Glu Asn Tyr Val Arg			
67	105	110	115	
69	tct cag ctg aat gcc aac atc aaa act ctg ttt gcc tta gga act cct	860		
70	Ser Gln Leu Asn Ala Asn Ile Lys Thr Leu Phe Ala Leu Gly Thr Pro			
71	120	125	130	
73	aat cca ctg gag gga gaa cta caa aga aaa ctg gct tgg gaa gat	908		
74	Asn Pro Leu Glu Gly Glu Leu Gln Arg Lys Leu Ala Trp Glu Asp			
75	135	140	145	150
77	caa agg tac aat gat ata att cag caa gac ttt gtt gat tct ttc tac	956		
78	Gln Arg Tyr Asn Asp Ile Ile Gln Gln Asp Phe Val Asp Ser Phe Tyr			
79	155	160	165	
81	aat ctt act ctg aaa tta ctt atg cag ttc agt tgg gca aat acc tat	1004		
82	Asn Leu Thr Leu Lys Leu Leu Met Gln Phe Ser Trp Ala Asn Thr Tyr			
83	170	175	180	
85	tgt cca cat gcc aaa ttt ctt atg act gct gat gac ata ttt att	1052		
86	Cys Pro His Ala Lys Phe Leu Met Thr Ala Asp Asp Asp Ile Phe Ile			
87	185	190	195	
89	cac atg cca aat ctg att gag tac ctt caa agt tta gaa caa att ggt	1100		
90	His Met Pro Asn Leu Ile Glu Tyr Leu Gln Ser Leu Glu Gln Ile Gly			
91	200	205	210	
93	gtt caa gac ttt tgg att ggt cgt gtt cat cgt ggt gcc cct ccc att	1148		
94	Val Gln Asp Phe Trp Ile Gly Arg Val His Arg Gly Ala Pro Pro Ile			
95	215	220	225	230
97	aga gat aaa agc agc aaa tac tac gtg tcc tat gaa atg tac cag tgg	1196		
98	Arg Asp Lys Ser Ser Lys Tyr Tyr Val Ser Tyr Glu Met Tyr Gln Trp			
99	235	240	245	
101	cca gct tac cct gac tac aca gcc gga gct gcc tat gta atc tcc ggt	1244		
102	Pro Ala Tyr Pro Asp Tyr Thr Ala Gly Ala Ala Tyr Val Ile Ser Gly			
103	250	255	260	
105	gat gta gct gcc aaa gtc tat gag gca tca cag aca cta aat tca agt	1292		
106	Asp Val Ala Ala Lys Val Tyr Glu Ala Ser Gln Thr Leu Asn Ser Ser			
107	265	270	275	
109	ctt tac ata gac gat gtg ttc atg ggc ctc tgt gcc aat aaa ata ggg	1340		
110	Leu Tyr Ile Asp Asp Val Phe Met Gly Leu Cys Ala Asn Lys Ile Gly			
111	280	285	290	
113	ata gta ccg cag gac cat gtg ttt tct gga gag ggt aaa act cct	1388		
114	Ile Val Pro Gln Asp His Val Phe Phe Ser Gly Glu Gly Lys Thr Pro			
115	295	300	305	310
117	tat cat ccc tgc atc tat gaa aaa atg atg aca tct cat gga cac tta	1436		
118	Tyr His Pro Cys Ile Tyr Glu Lys Met Met Thr Ser His Gly His Leu			
119	315	320	325	
121	gaa gat ctc cag gac ctt tgg aag aat gct aca gat cct aaa gta aaa	1484		
122	Glu Asp Leu Gln Asp Leu Trp Lys Asn Ala Thr Asp Pro Lys Val Lys			
123	330	335	340	
125	acc att tcc aaa ggt ttt ttt ggt caa ata tac tgc aga tta atg aag	1532		
126	Thr Ile Ser Lys Gly Phe Phe Gly Gln Ile Tyr Cys Arg Leu Met Lys			
127	345	350	355	

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181 <212> TYPE: PRT  
182 <213> ORGANISM: Homo sapiens  
184 <400> SEQUENCE: 2  
185 Met Arg Met Leu Val Ser Gly Arg Arg Val Lys Lys Trp Gln Leu Ile  
186 1 5 10 15  
187 Ile Gln Leu Phe Ala Thr Cys Phe Leu Ala Ser Leu Met Phe Phe Trp  
188 20 25 30  
189 Glu Pro Ile Asp Asn His Ile Val Ser His Met Lys Ser Tyr Ser Tyr  
190 35 40 45  
191 Arg Tyr Leu Ile Asn Ser Tyr Asp Phe Val Asn Asp Thr Leu Ser Leu  
192 50 55 60  
193 Lys His Thr Ser Ala Gly Pro Arg Tyr Gln Tyr Leu Ile Asn His Lys  
194 65 70 75 80  
195 Glu Lys Cys Gln Ala Gln Asp Val Leu Leu Leu Phe Val Lys Thr  
196 85 90 95  
197 Ala Pro Glu Asn Tyr Asp Arg Arg Ser Gly Ile Arg Arg Thr Trp Gly  
198 100 105 110  
199 Asn Glu Asn Tyr Val Arg Ser Gln Leu Asn Ala Asn Ile Lys Thr Leu  
200 115 120 125  
201 Phe Ala Leu Gly Thr Pro Asn Pro Leu Glu Gly Glu Leu Gln Arg  
202 130 135 140  
203 Lys Leu Ala Trp Glu Asp Gln Arg Tyr Asn Asp Ile Ile Gln Gln Asp  
204 145 150 155 160  
205 Phe Val Asp Ser Phe Tyr Asn Leu Thr Leu Lys Leu Leu Met Gln Phe  
206 165 170 175  
207 Ser Trp Ala Asn Thr Tyr Cys Pro His Ala Lys Phe Leu Met Thr Ala  
208 180 185 190  
209 Asp Asp Asp Ile Phe Ile His Met Pro Asn Leu Ile Glu Tyr Leu Gln  
210 195 200 205  
211 Ser Leu Glu Gln Ile Gly Val Gln Asp Phe Trp Ile Gly Arg Val His  
212 210 215 220  
213 Arg Gly Ala Pro Pro Ile Arg Asp Lys Ser Ser Lys Tyr Tyr Val Ser  
214 225 230 235 240  
215 Tyr Glu Met Tyr Gln Trp Pro Ala Tyr Pro Asp Tyr Thr Ala Gly Ala  
216 245 250 255  
217 Ala Tyr Val Ile Ser Gly Asp Val Ala Ala Lys Val Tyr Glu Ala Ser  
218 260 265 270  
219 Gln Thr Leu Asn Ser Ser Leu Tyr Ile Asp Asp Val Phe Met Gly Leu  
220 275 280 285  
221 Cys Ala Asn Lys Ile Gly Ile Val Pro Gln Asp His Val Phe Phe Ser  
222 290 295 300  
223 Gly Glu Gly Lys Thr Pro Tyr His Pro Cys Ile Tyr Glu Lys Met Met  
224 305 310 315 320  
225 Thr Ser His Gly His Leu Glu Asp Leu Gln Asp Leu Trp Lys Asn Ala  
226 325 330 335  
227 Thr Asp Pro Lys Val Lys Thr Ile Ser Lys Gly Phe Phe Gly Gln Ile  
228 340 345 350  
229 Tyr Cys Arg Leu Met Lys Ile Ile Leu Leu Cys Lys Ile Ser Tyr Val  
230 355 360 365

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231 Asp Thr Tyr Pro Cys Arg Ala Ala Phe Ile  
232 370 375  
235 <210> SEQ ID NO: 3  
236 <211> LENGTH: 1134  
237 <212> TYPE: DNA  
238 <213> ORGANISM: Homo sapiens  
240 <220> FEATURE:  
241 <221> NAME/KEY: CDS  
242 <222> LOCATION: (1)...(1134)  
244 <400> SEQUENCE: 3  
245 atg aga atg ttg gtt agt ggc aga aga gtc aaa aaa tgg cag tta att 48  
246 Met Arg Met Leu Val Ser Gly Arg Arg Val Lys Lys Trp Gln Leu Ile  
247 1 5 10 15  
249 att cag tta ttt gct act tgt ttt tta gcg agc ctc atg ttt ttt tgg 96  
250 Ile Gln Leu Phe Ala Thr Cys Phe Leu Ala Ser Leu Met Phe Phe Trp  
251 20 25 30  
253 gaa cca atc gat aat cac att gtg agc cat atg aag tca tat tct tac 144  
254 Glu Pro Ile Asp Asn His Ile Val Ser His Met Lys Ser Tyr Ser Tyr  
255 35 40 45  
257 aga tac ctc ata aat agc tat gac ttt gtg aat gat acc ctg tct ctt 192  
258 Arg Tyr Leu Ile Asn Ser Tyr Asp Phe Val Asn Asp Thr Leu Ser Leu  
259 50 55 60  
261 aag cac acc tca gcg ggg cct cgc tac caa tac ttg att aac cac aag 240  
262 Lys His Thr Ser Ala Gly Pro Arg Tyr Gln Tyr Leu Ile Asn His Lys  
263 65 70 75 80  
265 gaa aag tgt caa gct caa gac gtc ctc ctt tta ctg ttt gta aaa act 288  
266 Glu Lys Cys Gln Ala Gln Asp Val Leu Leu Leu Phe Val Lys Thr  
267 85 90 95  
269 gct cct gaa aac tat gat cga cgt tcc gga att aga agg acg tgg ggc 336  
270 Ala Pro Glu Asn Tyr Asp Arg Arg Ser Gly Ile Arg Arg Thr Trp Gly  
271 100 105 110  
273 aat gaa aat tat gtt cgg tct cag ctg aat gcc aac atc aaa act ctg 384  
274 Asn Glu Asn Tyr Val Arg Ser Gln Leu Asn Ala Asn Ile Lys Thr Leu  
275 115 120 125  
277 ttt gcc tta gga act cct aat cca ctg gag gga gaa gaa cta caa aga 432  
278 Phe Ala Leu Gly Thr Pro Asn Pro Leu Glu Gly Glu Leu Gln Arg  
279 130 135 140  
281 aaa ctg gct tgg gaa gat caa agg tac aat gat ata att cag caa gac 480  
282 Lys Leu Ala Trp Glu Asp Gln Arg Tyr Asn Asp Ile Ile Gln Gln Asp  
283 145 150 155 160  
285 ttt gtt gat tct ttc tac aat ctt act ctg aaa tta ctt atg cag ttc 528  
286 Phe Val Asp Ser Phe Tyr Asn Leu Thr Leu Lys Leu Leu Met Gln Phe  
287 165 170 175  
289 agt tgg gca aat acc tat tgt cca cat gcc aaa ttt ctt atg act gct 576  
290 Ser Trp Ala Asn Thr Tyr Cys Pro His Ala Lys Phe Leu Met Thr Ala  
291 180 185 190  
293 gat gat gac ata ttt att cac atg cca aat ctg att gag tac ctt caa 624  
294 Asp Asp Asp Ile Phe Ile His Met Pro Asn Leu Ile Glu Tyr Leu Gln  
295 195 200 205

**VERIFICATION SUMMARY**

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Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\09212001\I945254.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date